



# Blast 2 Sequences results

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Taxonomy

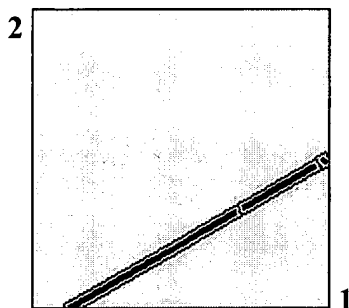
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq\_1 Length 666 (1 .. 666)

Sequence 2 lcl|seq\_2 Length 1162 (1 .. 1162)



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NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 987 bits (2552), Expect = 0.0

Identities = 498/589 (84%), Positives = 511/589 (86%), Gaps = 2/589 (0%)

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Query: 79  MVAIADARYDTSNDNSLIDTVAKYSVDDGETWETQIAIKNXXXXXXXXXXDPTVIVKGNK 138
          MVAIADARY+TS++NSLIDTVAKYSVDDGETWETQIAIKN          DPTVIVKGNK
Sbjct: 1   MVAIADARYETSSNSLIDTVAKYSVDDGETWETQIAIKNSRVSSVSRVVDPTVIVKGNK 60

Query: 139 LYVLVGXXXXXXXXXXXXHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA 198
          LYVLVG          HGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA
Sbjct: 61  LYVLVGSYSSRSYSSSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA 120

Query: 199 EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFYSKIFYSDDGKTWKFGKGRSD 258
          EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFYSKIFYSDDGKTWKFGKGRSD
Sbjct: 121 EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKRKQVFYSKIFYSDDGKTWKFGKGRSD 180

Query: 259 FGCSEPVALEWEGKLIINTRVDWKRRLLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS 318
          FGCSEPVALEWEGKLIINTRVDWKRRLLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS
Sbjct: 181 FGCSEPVALEWEGKLIINTRVDWKRRLLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS 240

Query: 319 QSSFTA VTIEGMRVMLFTHPLNFKGRWLRDRNLNLWLTDNQRIYNVGQVSI GDENSAYSSV 378
          Q+SFTA VTIEGMRVMLFTHPLNFKGR +RDRNLNLWLTDNQRIYNVGQVSI GDENSAYSSV
Sbjct: 241 QTSFTA VTIEGMRVMLFTHPLNFKGR CVRDRNLNLWLTDNQRIYNVGQVSI GDENSAYSSV 300

Query: 379 LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNWDSHLSSICTPADPAASS 438
          LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNW + +
Sbjct: 301 LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNWTATCPAFAPLLIQPLRR 360

Query: 439 SESGCGPAVTTVGLVGFLSGNASQNVWEDAYRCVNA STANAERVRNGLKFAGVGGGALWP 498
          P + L+ F + + +YRCVNA STANAERVRNGLKFAGVGGGALWP
  
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**EXHIBIT**

Sbjct: 361 QRVVVVPLSPRLVLLAFCRQRLPKRM-GGSYRCVNASTANAERVRNGLKFAGVGGGALWP 419

Query: 499 VSQQGQNQRYRFANHAFTLVASVTIHEAPRAASXXXXXXXXXXXXXXXXXXXXYDEKHQWQ 558  
VSQQGQNQRYRFANHAFTLVASVTIHEAPRAAS YDEKHQWQ

Sbjct: 420 VSQQGQNQRYRFANHAFTLVASVTIHEAPRAASPLLGASLDSSGGKKLLGLSYDEKHQWQ 479

Query: 559 PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY 618  
PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY

Sbjct: 480 PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY 539

Query: 619 VGGYKRSDMPTISHVTVNNVLLYN-RQLNTEEIRTLFLSQDLIGTEAHM 666  
VGGYKRSDMPTISHVTVNNVLLYN RQLNTEEIRTLFLSQDLIGTEAHM

Sbjct: 540 VGGYKRSDMPTISHVTVNNVLLYNRRQLNTEEIRTLFLSQDLIGTEAHM 588

CPU time: 0.17 user secs. 0.07 sys. secs 0.24 total secs.

Lambda	K	H
0.317	0.134	0.406

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Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 105,870

Number of Sequences: 0

Number of extensions: 556

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 666

length of database: 463,592,631

effective HSP length: 134

effective length of query: 532

effective length of database: 463,592,497

effective search space: 246631208404

effective search space used: 246631208404

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 78 (34.7 bits)